dampness-heat retention according to Traditional Chinese Medicine (TCM) theory.
Methods: A total of 96 patients who were HBsAg and HBVDNA positive and differentiated as TCM syndrome pattern of liver depression and spleen asthenia accompanied by dampness-heat retention were enrolled. They were randomized to receive either JianpiQinghua Prescription Combined with Lamivudine or lamivudine 100 mg daily or JianpiQinghua Prescription Rate of HBVDNA loss, change of HBVDNA load, indicators of liver function and symptoms and signs were observed in all patients for 2 years. HBVDNA drew from sera of patients who were HBVDNA positive at different periods of treatment of JianpiQinghua Prescription Combined with Lamivudine or lamivudine alone, were amplified by polymerase chain reaction, then adopted caliper1000 micro – slow chip technique to determine HBV YMDD mutants.
Results: At the end of the 2nd year, 81.3% of JianpiQinghua Prescription Combined with Lamivudine recipients had undetectable serum HBVDNA, compared with 48.4% and 40.0% of those in the lamivudine 100 mg daily or JianpiQinghua Prescription. Rate of HBeAg/anti-HBe seroconversion were 42.1% vs 23.8%.20.8%. ALT levels were remained in normal ranges in 96.3% and 71.4% of whose ALT were abnormal before treatment in the treated group and lamivudine control group respectively. At the end of the 2nd year, 93.8% vers 58.1% and 46.7% of patients in the treated group and the control groups respectively achieved total respond rate, there were significant difference between the three groups. By the end of 2 years, HBV YMDD mutation in the treated group was 15.6%, whereas lamivudine controlled group was 38.7%, there were significant difference between two groups. YMDD mutation in those precore nt1896 mutations seemed to higher than non-precore nt1896 mutations but there was no significant difference.The influence of HBV genotype to YMDD mutation had not been proved, the mean HBVDNA levels and serum ALT were higher in the YMDD mutations than those in non-YMDD mutations, but still lower than before treatment HBeAg/anti-HBe seroconversion occurred in the YMDD mutations but lower than non-YMDD mutations.
Conclusions: HBV replication and YMDD mutation suppressing as well as liver function and clinical improvement could be obtained after 2-years combination therapy of JianpiQinghua Prescription Combined with Lamivudine of good tolerance and safety. Affecting factors of hepatitis B virus (HBV) YMDD mutant related to Lamivudine were:long period of treatment, taller HBVDNA loads and lower level of serum ALT before treatment, HBeAg positive, higher body mass index. The better early virological response can be one of the significant predictors of curative effect for Lamivudine treatment.

PP-023 Enhancing the immune responses of HBsAg-pulsed DC vaccine to hepatitis B virus by blocking PD-1:PD-L1 signal

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Mechanisms underlying to chronic infection of hepatitis B virus are not well-understood. Impaired function of DCs in chronic viral infections has been reported, and recent reports showed that PD-1 and its cognate ligand PD-L1 interaction negatively modulates the immunity to T lymphocyte function. To investigate the immune responses of DC vaccine to hepatitis B virus after blocking PD-1:PD-L1 pathway with PD-L1 monoclonal neutralizing antibodies (Abs). We treated HBV transgenic mice (inbred BALB/c) with blocking Abs specific for PD-L1, followed by adoptive transfer of HBsAg-pulsed DCs, which were generated from BALB/c bone marrow cells.Three and six days after transfer, Blocking PD-L1 signaling stimulated proliferation of CD3+CD8+ splenic T lymphocytes more efficiently than DC vaccine treatment alone, coincident elevation of secreting IFN-γ, which was an important antiviral cytokine. In addition we found that the HBsAg titers in the serum of mice treated with PD-L1 Abs were dramatically decreased, which is accompanied with increased levels of ALT. These results indicate that blocking PD-1:PD-L1 interaction can promote the proliferation of specific CD3+CD8+ T lymphocytes proliferation and stimulate the secretion of IFN-γ, which synergistically improves the function of inhibiting HBV in transgenic mice induced by HBsAg-pulsed DC vaccine. DCs pulsed by HBsAg in combination with anti-PD-L1 Abs thus may be a promising approach for therapeutic vaccination to hepatitis B virus.

PP-024 Tumor necrosis factor-α-308 gene promoter polymorphism in chronic hepatitis B virus infection: Evidence from 22 studies

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Background: Tumor necrosis factor-α (TNF-α) plays a pivotal role in the viral clearance and host immune response to HBV, and the capacity for TNF-α production in individuals is influenced by a major genetic component. The studies of TNF-α-308 gene promoter polymorphism in chronic HBV infection have reported apparently conflicting results.
Objective: We did meta-analysis on TNF-α genetic variants to derive a more precise estimation of the relationship between the polymorphism of TNF-α-308 gene promoter and chronic HBV infection.
Method: Meta-analysis was done of 22 case-control studies in relation to TNF-α-308 gene promoter, involving a total of 4338 chronic HBV infection cases and 3013 controls. The pooled odds ratios (ORs) for the risk associated with the genotypes of GA, AA, and GA+AA (A-allele carriers) compared with the GG genotype were calculated.
Results: Overall meta-analysis indicated that −308A heterozygotes (GA) had a roughly 22% decreased risk of developing CHB with a borderline significance (OR = 0.78; 95% CI: 0.60–1.02; $P = 0.065$). For the −308A allele homozygotes (AA) and carriers (GA+AA), the pooled ORs both indicated a significantly decreased risk of CHB (OR = 0.39; 95% CI: 0.21–0.73; $P = 0.003$; and OR = 0.74; 95% CI: 0.57–0.96; $P = 0.026$, respectively) (Table 1). In the subgroup analyses by ethnicity, significantly decreased risks were associated with −308 variant genotypes (GA and AA) in Mongoloid populations in all genetic models. However, no significant associations were found in Caucasoid.
Conclusion: The meta-analysis suggests that the TNF-α–308A allele is a low-penetrant protective factor for chronic HBV infection, especially in Mongoloid.

Table 1. Main results of pooled ORs in the meta-analysis

	GA vs GG			AA vs GG			GA + AA vs GG		
	OR (95%CI)	*P*	*P* (Q-test)	OR (95%CI)	*P*	*P* (Q-test)	OR (95%CI)	*P*	*P* (Q-test)
Total	0.78 (0.60, 1.02)	0.065	0.0001	0.39 (0.21, 0.73)	0.003	0.094	0.74 (0.57, 0.96)	0.026	0.0001
Mongoloid	0.71 (0.49, 1.04)	0.078	0.0001	0.18 (0.11, 0.31)	0.0001	0.440	0.66 (0.46, 0.95)	0.026	0.0001
Caucasoid	0.91 (0.73, 1.14)	0.408	0.185	0.93 (0.43, 1.99)	0.842	0.672	0.91 (0.73, 1.13)	0.409	0.121
SR	0.67 (0.50, 0.89)	0.006	0.080	0.31 (0.17, 0.54)	0.0001	0.159	0.65 (0.49, 0.86)	0.003	0.062
Healthy	0.88 (0.59, 1.34)	0.559	0.0001	0.40 (0.16, 1.01)	0.054	0.098	0.82 0.54, 1.24)	0.347	0.0001

Note: *P*(Q-test): *P* value of Q-test for heterogeneity test.
A random-effects model was used when *P* value for heterogeneity test <0.1; otherwise, a fixed-effects model was used.